



## SEQUENCE LISTING

<10> Lukyanov, Sergey  
 Lukyanov, Konstantin  
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 Savistky, Alexandr  
 Fradkov, Arcady

<120> Non Aggregating Fluorescent Proteins and  
 Methods for Using the Same

<130> CLON-067

<140> 10/081,864

<141> 2002-02-20

<150> 10/006,922

<151> 2001-12-04

<150> 60/270,983

<151> 2001-02-21

<160> 30

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 687

<212> DNA

<213> Anemonia majano

<400> 1

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tgtgtcaatg ggcattactt taccgtcaaa ggtgaaggca acgggaagcc atacgaaggg 120
acgcagacct cgacttttaa agtcaccatg gccaacggtg ggccccttgc attctccttt 180
gacatactat ctacagtgtt caagtatgga aatcgatgct ttactgcgta tcctaccagt 240
atgcccgact atttcaaaca agcatttcct gacggaatgt catatgaaag gacttttacc 300
tatgaagatg gaggagttgc tacagccagt tgggaaataa gccttaaagg caactgcttt 360
gagcacaat ccacgtttca tggagtgaac tttcctgctg atggacctgt gatggcgaag 420
atgacaactg gttgggaccc atcttttgag aaaatgactg tctgcgatgg aatattgaag 480
ggtgatgtca ccgcgttcct catgctgcaa ggaggtggca attacagatg ccaattccac 540
acttcttaca agacaaaaaa accggtgacg atgccaccaa accatgcggt ggaacatcgc 600
attgcgagga ccgaccttga caaaggtggc aacagtgttc agctgacgga gcacgctgtt 660
gcacatataa cctctgttgt ccctttc                                     687

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<210> 2

<211> 229

<212> PRT

<213> Anemonia majano

<400> 2

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 1          5          10          15
His Met Asp Gly Cys Val Asn Gly His Tyr Phe Thr Val Lys Gly Glu
 20          25          30
Gly Asn Gly Lys Pro Tyr Glu Gly Thr Gln Thr Ser Thr Phe Lys Val
 35          40          45
Thr Met Ala Asn Gly Gly Pro Leu Ala Phe Ser Phe Asp Ile Leu Ser
 50          55          60
Thr Val Phe Lys Tyr Gly Asn Arg Cys Phe Thr Ala Tyr Pro Thr Ser
 65          70          75          80
Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr Glu
 85          90          95
Arg Thr Phe Thr Tyr Glu Asp Gly Gly Val Ala Thr Ala Ser Trp Glu
100          105          110
Ile Ser Leu Lys Gly Asn Cys Phe Glu His Lys Ser Thr Phe His Gly
115          120          125
Val Asn Phe Pro Ala Asp Gly Pro Val Met Ala Lys Met Thr Thr Gly
130          135          140
Trp Asp Pro Ser Phe Glu Lys Met Thr Val Cys Asp Gly Ile Leu Lys
145          150          155          160
Gly Asp Val Thr Ala Phe Leu Met Leu Gln Gly Gly Gly Asn Tyr Arg
165          170          175
Cys Gln Phe His Thr Ser Tyr Lys Thr Lys Lys Pro Val Thr Met Pro
180          185          190
Pro Asn His Ala Val Glu His Arg Ile Ala Arg Thr Asp Leu Asp Lys
195          200          205
Gly Gly Asn Ser Val Gln Leu Thr Glu His Ala Val Ala His Ile Thr
210          215          220
Ser Val Val Pro Phe
225
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<210> 3

<211> 693

<212> DNA

<213> Zoanthus sp.

<400> 3

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aaacaggcta ttaatctgtg tgtggtcgaa ggtggaccat tgccatttgc cgaagacata 180
ttgtcagctg cctttatgta cggaaacagg gttttcactg aatatacctca agacatagct 240
gactatttca agaactcgtg tcctgctggt tatacatggg acaggctctt tctctttgag 300
gatggagcag tttgcatatg taatgcagat ataacagtga gtgttgaaga aaactgcatg 360
tatcatgagt ccaaatttta tggagtgaat tttctgctg atggacctgt gatgaaaaag 420
atgacagata actgggagcc atcctgcgag aagatcatac cagtacctaa gcaggggata 480
ttgaaagggg atgtctccat gtacctcctt ctgaaggatg gtgggcgttt acgggtgcca 540
ttcgacacag tttaaaaagc aaagtctgtg ccaagaaaga tgccggactg gcacttcac 600
cagcataagc tcacccgtga agaccgcagc gatgctaaga atcagaaatg gcatctgaca 660
gaacatgcta ttgcatccgg atctgcattg ccc 693
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<210> 4  
 <211> 231  
 <212> PRT  
 <213> Zoanthus sp.

<400> 4  
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 1 5 10 15  
 Arg Met Glu Gly Cys Val Asp Gly His Lys Phe Val Ile Thr Gly Glu  
 20 25 30  
 Gly Ile Gly Tyr Pro Phe Lys Gly Lys Gln Ala Ile Asn Leu Cys Val  
 35 40 45  
 Val Glu Gly Gly Pro Leu Pro Phe Ala Glu Asp Ile Leu Ser Ala Ala  
 50 55 60  
 Phe Asn Tyr Gly Asn Arg Val Phe Thr Glu Tyr Pro Gln Asp Ile Ala  
 65 70 75 80  
 Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Asp Arg Ser  
 85 90 95  
 Phe Leu Phe Glu Asp Gly Ala Val Cys Ile Cys Asn Ala Asp Ile Thr  
 100 105 110  
 Val Ser Val Glu Glu Asn Cys Met Tyr His Glu Ser Lys Phe Tyr Gly  
 115 120 125  
 Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Asp Asn  
 130 135 140  
 Trp Glu Pro Ser Cys Glu Lys Ile Ile Pro Val Pro Lys Gln Gly Ile  
 145 150 155 160  
 Leu Lys Gly Asp Val Ser Met Tyr Leu Leu Leu Lys Asp Gly Gly Arg  
 165 170 175  
 Leu Arg Cys Gln Phe Asp Thr Val Tyr Lys Ala Lys Ser Val Pro Arg  
 180 185 190  
 Lys Met Pro Asp Trp His Phe Ile Gln His Lys Leu Thr Arg Glu Asp  
 195 200 205  
 Arg Ser Asp Ala Lys Asn Gln Lys Trp His Leu Thr Glu His Ala Ile  
 210 215 220  
 Ala Ser Gly Ser Ala Leu Pro  
 225 230

<210> 5  
 <211> 865  
 <212> DNA  
 <213> Zoanthus sp.

<400> 5  
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 catgggtcat tcaaaacacg gtctaaaaga agaaatgaca atgaaatacc acatggaagg 120  
 gtgcgtcaac ggacataaat ttgtgatcac gggcgaaggc attggatatc cgttcaaagg 180  
 gaaacagact attaattctgt gtgtgatcga agggggacca ttgccatttt ccgaagacat 240  
 attgtcagct ggctttaagt acggagacag gatttttact gaatatcctc aagacatagt 300  
 agactatttc aagaactcgt gtctgtctgg atatacatgg ggcaggtctt ttctctttga 360  
 ggatggagca gtctgcatat gcaatgtaga tataacagtg agtgtcaaag aaaactgcat 420

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ttatcataag agcatattta atggaatgaa ttttcctgct gatggacctg tgatgaaaaa 480
gatgacaact aactgggaag catcctgcga gaagatcatg ccagtaccta agcaggggat 540
actgaaaggg gatgtctcca tgtacctcct tctgaaggat ggtgggcggt accggtgccca 600
gttcgacaca gttttacaaag caaagtctgt gccaaagtaag atgccggagt ggcacttcat 660
ccagcataag ctccctccgtg aagaccgcag cgatgctaag aatcagaagt ggcagctgac 720
agagcatgct attgcattcc cttctgcctt ggcctgataa gaatgtagtt ccaacatttt 780
aatgcatgtg cttgtcaatt attctgataa aaatgtagtt gagttgaaaa cagacaagta 840
caaataaagc acatgtaaat cgtct
865

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<210> 6
<211> 230
<212> PRT
<213> Zoanthus sp.

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<400> 6
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1 5 10 15
His Met Glu Gly Cys Val Asn Gly His Lys Phe Val Ile Thr Gly Glu
20 25 30
Gly Ile Gly Tyr Pro Phe Lys Gly Lys Gln Thr Ile Asn Leu Cys Val
35 40 45
Ile Glu Gly Gly Pro Leu Pro Phe Ser Glu Asp Ile Leu Ser Ala Gly
50 55 60
Phe Lys Tyr Gly Asp Arg Ile Phe Thr Glu Tyr Pro Gln Asp Ile Val
65 70 75 80
Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Gly Ser Phe
85 90 95
Leu Phe Glu Asp Gly Ala Val Cys Ile Cys Asn Val Asp Ile Thr Val
100 105 110
Ser Val Lys Glu Asn Cys Ile Tyr His Lys Ser Ile Phe Asn Gly Met
115 120 125
Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Thr Asn Trp
130 135 140
Glu Ala Ser Cys Glu Lys Ile Met Pro Val Pro Lys Gln Gly Ile Leu
145 150 155 160
Lys Gly Asp Val Ser Met Tyr Leu Leu Leu Lys Asp Gly Gly Arg Tyr
165 170 175
Arg Cys Gln Phe Asp Thr Val Tyr Lys Ala Lys Ser Val Pro Ser Lys
180 185 190
Met Pro Glu Trp His Phe Ile Gln His Lys Leu Leu Arg Glu Asp Arg
195 200 205
Ser Asp Ala Lys Asn Gln Lys Trp Gln Leu Thr Glu His Ala Ile Ala
210 215 220
Phe Pro Ser Ala Leu Ala
225 230

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<210> 7
<211> 678
<212> DNA
<213> Discosoma sp

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<400> 7

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atgcgctcct ccaagaacgt catcaaggag ttcatgcgct tcaaggtgcg catggagggc 60
accgtgaacg gccacgagtt cgagatcgag ggcgagggcg agggccgccc ctacgagggc 120
cacaacaccg tgaagctgaa ggtgaccaag ggcggccccc tgcccttcgc ctgggacatc 180
ctgtccccc agttccagta cggctccaag gtgtacgtga agcaccgccg cgacatcccc 240
gactacaaga agctgtcctt ccccgagggc ttcaagtggg agcgcgatgat gaacttcgag 300
gacggcgggc tgggtgaccgt gacccaggac tcctccctgc aggacggctg cttcatctac 360
aaggtgaagt tcacggcgt gaacttcccc tccgacggcc ccgtgatgca gaagaagacc 420
atgggctggg aggcctccac cgagcgcttg taccgccgag acggcgatgct gaagggcgag 480
atccacaagg ccctgaagct gaaggacggc ggccactacc tgggtggagtt caagtccatc 540
tacatggcca agaagcccgt gcagctgccc ggctactact acgtggactc caagctggac 600
atcacctccc acaacgagga ctacaccatc gtggagcagt acgagcgcac cgagggccgc 660
caccacctgt tcctgtaa
678

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<210> 8

<211> 225

<212> PRT

<213> Discosoma sp.

<400> 8

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Met Arg Ser Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys Val
1      5      10      15
Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu
20     25     30
Gly Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys Leu Lys Val
35     40     45
Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln
50     55     60
Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro
65     70     75     80
Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val
85     90     95
Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser
100    105    110
Leu Gln Asp Gly Cys Phe Ile Tyr Lys Val Lys Phe Ile Gly Val Asn
115    120    125
Phe Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu
130    135    140
Ala Ser Thr Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Glu
145    150    155    160
Ile His Lys Ala Leu Lys Leu Lys Asp Gly Gly His Tyr Leu Val Glu
165    170    175
Phe Lys Ser Ile Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Tyr
180    185    190
Tyr Tyr Val Asp Ser Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr
195    200    205
Thr Ile Val Glu Gln Tyr Glu Arg Thr Glu Gly Arg His His Leu Phe
210    215    220
Leu
225

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<210> 9  
 <211> 696  
 <212> DNA  
 <213> Anemonia sulcata

<400> 9  
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 ggccactact tcaagtgtac aggaaaagga gagggcaacc catttgaggg tacgcaggaa 120  
 atgaagatag aggtcatcga aggaggtcca ttgccatttg ccttcacat tttgtcaacg 180  
 agttgtatgt acggtagtaa ggccttcacg aagtatgtgt caggaattcc tgactacttc 240  
 aagcagtctt tccctgaagg ttttacttgg gaaagaacca caacctacga ggatggaggc 300  
 tttcttacag ctcacacagga cacaagccta gatggagatt gcctcgttta caaggtcaag 360  
 attcttggtg ataattttcc tgctgatggc cccgtgatgc agaacaaagc aggaagatgg 420  
 gagccatcca ccgagatagt ttatgaagtt gacgggtgcc tgcgtggaca gtctttgatg 480  
 gcccttaagt gccctggtgg tcgtcatctg acttgccatc tccatactac ttacaggtcc 540  
 aaaaaaccag ctgctgcctt gaagatgccg ggatttcatt ttgaagatca tcgcatcgag 600  
 ataatggagg aagttgagaa aggcaagtgc tataaacagt acgaagcagc agtgggcagg 660  
 tactgtgatg ctgctccatc caagcttgga cataac 696

<210> 10  
 <211> 232  
 <212> PRT  
 <213> Anemonia sulcata

<400> 10  
 Met Ala Ser Phe Leu Lys Lys Thr Met Pro Phe Lys Thr Thr Ile Glu  
 1 5 10 15  
 Gly Thr Val Asn Gly His Tyr Phe Lys Cys Thr Gly Lys Gly Glu Gly  
 20 25 30  
 Asn Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly  
 35 40 45  
 Gly Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr  
 50 55 60  
 Gly Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe  
 65 70 75 80  
 Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr  
 85 90 95  
 Glu Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly  
 100 105 110  
 Asp Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala  
 115 120 125  
 Asp Gly Pro Val Met Gln Asn Lys Ala Gly Arg Trp Glu Pro Ala Thr  
 130 135 140  
 Glu Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met  
 145 150 155 160  
 Ala Leu Lys Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr  
 165 170 175  
 Thr Tyr Arg Ser Lys Lys Pro Ala Ala Ala Leu Lys Met Pro Gly Phe  
 180 185 190  
 His Phe Glu Asp His Arg Ile Glu Ile Met Glu Glu Val Glu Lys Gly  
 195 200 205

Lys Cys Tyr Lys Gln Tyr Glu Ala Ala Val Gly Arg Tyr Cys Asp Ala  
 210 215 220  
 Ala Pro Ser Lys Leu Gly His Asn  
 225 230

<210> 11  
 <211> 678  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> hybrid coding sequence

<400> 11  
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 accgtgaacg gccacgagtt cgagatcaag ggcgagggcg agggccggcc ctacgagggc 120  
 cactgcagcg tgaagctcat ggtgaccaag ggcggccccc tccccttcgc cttcgacatc 180  
 ctcagccccc agttccagta cggcagcaag gtgtacgtga agcaccgccg cgacatcccc 240  
 gactacaaga agctcagctt ccccgagggc ttcaagtggg agcgggtgat gaacttcgag 300  
 gacggcgggc tgggtgaccgt gagccaggac agcagcctca aggacggctg cttcatctac 360  
 gaggtgaagt tcatcggcgt gaacttcccc agcagcggcc ccgtgatgca gcggcgggacc 420  
 cggggctggg aggccagcag cgagcggctc taccgccggg acggcggtgct caagggcgac 480  
 atccacatgg ccctccggct cgagggcggc ggccactacc tcgtggagtt caagagcatc 540  
 tacatggcca agaagcccgt gcagctcccc ggctactact acgtggacag caagctcgac 600  
 atcaccagcc acaacgagga ctacaccatc gtggagcagt acgagcggac cgagggccgg 660  
 caccacctct tcctctga 678

<210> 12  
 <211> 225  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> hybrid protein

<400> 12  
 Met Ser Cys Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys Val  
 1 5 10 15  
 Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Lys Gly Glu  
 20 25 30  
 Gly Glu Gly Arg Pro Tyr Glu Gly His Cys Ser Val Lys Leu Met Val  
 35 40 45  
 Thr Lys Gly Gly Pro Leu Pro Phe Ala Phe Asp Ile Leu Ser Pro Gln  
 50 55 60  
 Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro  
 65 70 75 80  
 Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val  
 85 90 95  
 Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Ser Gln Asp Ser Ser  
 100 105 110

Leu	Lys	Asp	Gly	Cys	Phe	Ile	Tyr	Glu	Val	Lys	Phe	Ile	Gly	Val	Asn
		115					120					125			
Phe	Pro	Ser	Asp	Gly	Pro	Val	Met	Gln	Arg	Arg	Thr	Arg	Gly	Trp	Glu
	130					135					140				
Ala	Ser	Ser	Glu	Arg	Leu	Tyr	Pro	Arg	Asp	Gly	Val	Leu	Lys	Gly	Asp
145					150					155					160
Ile	His	Met	Ala	Leu	Arg	Leu	Glu	Gly	Gly	Gly	His	Tyr	Leu	Val	Glu
			165					170						175	
Phe	Lys	Ser	Ile	Tyr	Met	Ala	Lys	Lys	Pro	Val	Gln	Leu	Pro	Gly	Tyr
		180						185				190			
Tyr	Tyr	Val	Asp	Ser	Lys	Leu	Asp	Ile	Thr	Ser	His	Asn	Glu	Asp	Tyr
	195					200						205			
Thr	Ile	Val	Glu	Gln	Tyr	Glu	Arg	Thr	Glu	Gly	Arg	His	His	Leu	Phe
	210					215					220				

Leu  
225

<210> 13  
 <211> 675  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> non-aggregating mutant

<400> 13  
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 accgtgaacg gccacgagtt cgagatcgag ggcgagggcg agggccgccc ctacgagggc 120  
 cacaacaccg tgaagctgaa ggtgaccaag ggcgggcccc tgcccttcgc ctgggacatc 180  
 ctgtcccccc agttccagta cggctccaag gtgtacgtga agcacccegc cgacatcccc 240  
 gactacaaga agctgtcctt ccccgagggc ttcaagtggg agcgcgtgat gaacttcgag 300  
 gacggcgggc tggcgaccgt gaccacggac tcctccctgc aggacggctg cttcatctac 360  
 aaggtgaagt tcacggcgt gaacttcccc tccgacggcc ccgtgatgca gaagaagacc 420  
 atgggctggg aggcctccac cgagcgcttg tacccecgcg acggcgtgct gaagggcgag 480  
 acccacaagg ccttgaagct gaaggacggc ggccactacc tgggtggagt caagtccatc 540  
 tacatggcca agaagcccgt gcagctgccc ggctactact acgtggacgc caagctggac 600  
 atcacctccc acaacgagga ctacaccatc gtggagcagt acgagcgcac cgagggccgc 660  
 caccacctgt tcctg 675

<210> 14  
 <211> 678  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> non-aggregating mutant

<400> 14  
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 accgtgaacg gccacgagtt cgagatcgag ggcgagggcg agggccgccc ctacgagggc 120



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cacaacaccg tgaagttgaa ggtgaccaag ggcggccccc tgcccttcgc ctgggacatc 180
ctgtccccc agttccagta cggctccaag gtgtacgtga agcaccgcc cgacatcccc 240
gactacaaga agctgtcctt ccccgagggc ttcaagtggg agcgcgtgat gaacttcgag 300
gacggcggcg tggcgaccgt gaccagggac tcctccctgc aggacggctg cttcatctac 360
aaggtgaagt tcatcggcgt gaacttcccc tccgacggcc ccgtgatgca gaagaagacc 420
atgggctggg aggctccac cgagcgctg taccgccgcg acggcgtgct gaagggcgag 480
atccacaagg ccctgaagct gaaggacggc ggccactacc tgggtggagt caagtccatc 540
tacatggcca agaagcccg gcagctgccc ggctactact acgtggacac caagtggac 600
atcacctccc acaacgagga ctacaccatc gtggagcagt acgagcgcac cgagggccgc 660
caccacctgt tcctgtaa
678

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<210> 15

<211> 705

<212> DNA

<213> Artificial Sequence

<220>

<223> non-aggregating mutant

<400> 15

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gggaaacagg ctattaatct gtgtgtggtc gaagggtggac cattgccatt tgccgaagac 180
atattgtcag ctgcctttat gtacggaaac agggttttca ctgaatatcc tcaagacata 240
gttgactatt tcaagaactc gtgtcctgct ggatatacat gggacaggtc ttttctcttt 300
gaggatggag cagtttgcac atgtaatgca gatataacag tgagtgttga agaaaactgc 360
atgtatcatg agtccaaatt ctatggagtg aattttcctg ctgatggacc tgtgatgaaa 420
aagatgacag ataactggga gccatcctgc gagaagatca taccagtacc taagcagggg 480
atattgaaag gggatgtctc catgtacctc cttctgaagg atgggtggcg ttacgggtgc 540
caattcgaca cagtttacaa agcaaaagtct gtgccaaaga agatgccgga ctggcacttc 600
atccagcata agctaccccg tgaagaccgc agcgatgcta agaatacaga atggcatctg 660
acagaacatg ctattgcatc cggatctgca ttgccctgaa agctt
705

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<210> 16

<211> 230

<212> PRT

<213> Artificial Sequence

<220>

<223> non-aggregating mutant

<400> 16

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Ala His Ser Glu His Gly Leu Thr Glu Glu Met Thr Met Lys Tyr His
1           5           10           15
Met Glu Gly Cys Val Asn Gly His Lys Phe Val Ile Thr Gly Glu Gly
20           25           30
Ile Gly Tyr Pro Phe Lys Gly Lys Gln Thr Ile Asn Leu Cys Val Ile
35           40           45
Glu Gly Gly Pro Leu Pro Phe Ser Glu Asp Ile Leu Ser Ala Gly Phe
50           55           60
Lys Tyr Gly Asp Arg Ile Phe Thr Glu Tyr Pro Gln Asp Ile Val Asp

```

65					70					75				80	
Tyr	Phe	Lys	Asn	Ser	Cys	Pro	Ala	Gly	Tyr	Thr	Trp	Gly	Arg	Ser	Phe
				85					90					95	
Leu	Phe	Glu	Asp	Gly	Ala	Val	Cys	Ile	Cys	Asn	Val	Asp	Ile	Thr	Val
			100					105					110		
Ser	Val	Lys	Glu	Asn	Cys	Ile	Tyr	His	Lys	Ser	Ile	Phe	Asn	Gly	Val
		115					120					125			
Asn	Phe	Pro	Ala	Asp	Gly	Pro	Val	Met	Lys	Lys	Met	Thr	Thr	Asn	Trp
		130				135					140				
Glu	Ala	Ser	Cys	Glu	Lys	Ile	Met	Pro	Val	Pro	Lys	Gln	Gly	Ile	Leu
145					150					155				160	
Lys	Gly	Asp	Val	Ser	Met	Tyr	Leu	Leu	Leu	Lys	Asp	Gly	Gly	Arg	Tyr
			165					170						175	
Arg	Cys	Gln	Phe	Asp	Thr	Val	Tyr	Lys	Ala	Lys	Ser	Val	Pro	Ser	Lys
		180					185					190			
Met	Pro	Glu	Trp	His	Phe	Ile	Gln	His	Lys	Leu	Leu	Arg	Glu	Asp	Arg
	195					200					205				
Ser	Asp	Ala	Lys	Asn	Gln	Lys	Trp	Gln	Leu	Thr	Glu	His	Ala	Ile	Ala
	210				215						220				
Phe	Pro	Ser	Ala	Leu	Ala										
225					230										

<210> 17  
 <211> 705  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> non-aggregating mutant

<400> 17  
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 ggctgcgtga acggccacaa gttcgtgatc accggcgagg gcatcggcta ccccttcaag 120  
 ggcaagcaga ccatcaacct gtgcgtgatc gaggggcgcc ccctgccctt cagcgaggac 180  
 atcctgagcg ccggcttcaa gtacggcgac cggatcttca ccgagtaccc ccaggacatc 240  
 gtggactact tcaagaacag ctgccccgcc ggctacacct gggggccggag ctccctgttc 300  
 gaggacggcg ccgtgtgcat ctgtaacgtg gacatcaccc tgagcgtgaa ggagaactgc 360  
 atctaccaca agagcatctt caacggcgtg aacttccccg ccgacggccc cgtgatgaag 420  
 aagatgacca ccaactggga ggccagctgc gagaagatca tgcccgtgcc taagcagggc 480  
 atcctgaagg gcgacgtgag catgtacctg ctgctgaagg acggcgggcc gtaccggtgc 540  
 cagttcgaca ccgtgtacaa ggccaagagc gtgcccagca agatgcccga gtggcacttc 600  
 atccagcaca agctgctgcg ggaggaccgg agcgacgcca agaaccagaa gtggcagctg 660  
 accgagcacg ccatcgccctt ccccgacgcc ctggcctgaa agctt 705

<210> 18  
 <211> 230  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> non-aggregating mutant

<400> 18

Ala	His	Ser	Glu	His	Gly	Leu	Thr	Glu	Glu	Met	Thr	Met	Lys	Tyr	His
1				5					10					15	
Met	Glu	Gly	Cys	Val	Asn	Gly	His	Lys	Phe	Val	Ile	Thr	Gly	Glu	Gly
			20					25					30		
Ile	Gly	Tyr	Pro	Phe	Lys	Gly	Lys	Gln	Thr	Ile	Asn	Leu	Cys	Val	Ile
		35					40					45			
Glu	Gly	Gly	Pro	Leu	Pro	Phe	Ser	Glu	Asp	Ile	Leu	Ser	Ala	Gly	Phe
	50					55					60				
Lys	Tyr	Gly	Asp	Arg	Ile	Phe	Thr	Glu	Tyr	Pro	Gln	Asp	Ile	Val	Asp
65					70					75				80	
Tyr	Phe	Lys	Asn	Ser	Cys	Pro	Ala	Gly	Tyr	Thr	Trp	Gly	Arg	Ser	Phe
			85					90					95		
Leu	Phe	Glu	Asp	Gly	Ala	Val	Cys	Ile	Cys	Asn	Val	Asp	Ile	Thr	Val
			100					105					110		
Ser	Val	Lys	Glu	Asn	Cys	Ile	Tyr	His	Lys	Ser	Ile	Phe	Asn	Gly	Val
		115					120					125			
Asn	Phe	Pro	Ala	Asp	Gly	Pro	Val	Met	Lys	Lys	Met	Thr	Thr	Asn	Trp
	130					135					140				
Glu	Ala	Ser	Cys	Glu	Lys	Ile	Met	Pro	Val	Pro	Lys	Gln	Gly	Ile	Leu
145					150					155				160	
Lys	Gly	Asp	Val	Ser	Met	Tyr	Leu	Leu	Leu	Lys	Asp	Gly	Gly	Arg	Tyr
			165					170						175	
Arg	Cys	Gln	Phe	Asp	Thr	Val	Tyr	Lys	Ala	Lys	Ser	Val	Pro	Ser	Lys
			180					185					190		
Met	Pro	Glu	Trp	His	Phe	Ile	Gln	His	Lys	Leu	Leu	Arg	Glu	Asp	Arg
		195					200					205			
Ser	Asp	Ala	Lys	Asn	Gln	Lys	Trp	Gln	Leu	Thr	Glu	His	Ala	Ile	Ala
	210					215					220				
Phe	Pro	Ser	Ala	Leu	Ala										
225					230										

<210> 19

<211> 690

<212> DNA

<213> Artificial Sequence

<220>

<223> non-aggregating mutant

<400> 19

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atggcctgt ccaacgagtt catcggcgac gacatgaaga tgacctacca catggacggc 60
tgcgtaacg gccactactt caccgtgaag ggcgagggca gcggcaagcc ctacgagggc 120
accagacct ccaccttcaa ggtgaccatg gccaacggcg gcccctggc cttctccttc 180
gacatcctgt ccaccgtggt catgtacggc aacgctgct tcaccgccta cccaccagc 240
atgcccgact acttcaagca ggccttcccc gacggcatgt cctacgagag aaccttcacc 300
tacgaggacg gcggcggtggc caccgccagc tgggagatca gcctgaaggg caactgcttc 360
gagcacaagt ccaccttcca cggcggtgaac ttccccgccg acggccccgt gatggccaag 420
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<220>

<223> non-aggregating mutant

<400> 21

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ggatccgcct ccctgctgac cgagaccatg cccttcagga ccaccatcga gggcaccgtg 60
aacggccact acttcaagtg caccggcaag ggcgagggca accccctcga gggcacccag 120
gagatgaaga tcgaggtgat cgagggcggc cccctgccct tcgccttcca catcctgtcc 180
acctcctgca tgtacggctc caaggccttc atcaagtacg tgtccggcat ccccgactac 240
ttcaagcagt ccctccccga gggcttcacc tgggagcgca ccaccaccta cgaggacggc 300
ggcttcctga cgcgccacca ggacacctcc ctggacggcg actgcctggt gtacaagggtg 360
aagatcctgg gcaacaactt ccccgccgac ggccccgtga tgcagaacaa ggccggccgc 420
tgggagccct ccaccgagat cgtgtacgag gtggacggcg tgctgcgcgg ccagtccctg 480
atggccctgg agtgccccgg cggtcgccac ctgacctgcc acctgcacac cacctaccgc 540
tccaagaagc cgcctccgc cctgaagatg cccggcttcc acttcgagga ccaccgcac 600
gagatcctgg aggaggtgga gaagggcaag tgctacaagc agtacgaggc cgccgtgggc 660
cgctactgcg acgccgcccc ctccaagctg ggccacaact gaagctt 707
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<210> 22

<211> 231

<212> PRT

<213> Artificial Sequence

<220>

<223> non-aggregating mutant

<400> 22

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Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Arg Thr Thr Ile Glu Gly
1           5           10           15
Thr Val Asn Gly His Tyr Phe Lys Cys Thr Gly Lys Gly Glu Gly Asn
20           25           30
Pro Leu Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly
35           40           45
Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly
50           55           60
Ser Lys Ala Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys
65           70           75           80
Gln Ser Leu Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu
85           90           95
Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp
100          105          110
Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp
115          120          125
Gly Pro Val Met Gln Asn Lys Ala Gly Arg Trp Glu Pro Ser Thr Glu
130          135          140
Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met Ala
145          150          155          160
Leu Glu Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr Thr
165          170          175
Tyr Arg Ser Lys Lys Pro Ala Ser Ala Leu Lys Met Pro Gly Phe His
180          185          190
Phe Glu Asp His Arg Ile Glu Ile Leu Glu Glu Val Glu Lys Gly Lys
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	195		200		205										
Cys	Tyr	Lys	Gln	Tyr	Glu	Ala	Ala	Val	Gly	Arg	Tyr	Cys	Asp	Ala	Ala
	210					215					220				
Pro	Ser	Lys	Leu	Gly	His	Asn									
225					230										

<210> 23  
 <211> 654  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> non-aggregating mutant

<400> 23  
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 gagggcaccc aggagatgaa gatcgaggtg atcgagggcg gccccctgcc cttcgccttc 120  
 cacatcctgt ccacctcctg catgtacggc tccaaggcct tcatcaagta cgtgtccggc 180  
 atccccgact acttcaagca gtccctcccc gagggcttca cctgggagcg caccaccacc 240  
 tacgaggacg gcggcttcct gaccgcccac caggacacct ccctggacgg cgactgcctg 300  
 gtgtacaagg tgaagatcct gggcaacaac ttccccgccg acggccccgt gatgcagaac 360  
 aaggccggcc gctgggagcc ctccaccgag atcgtgtacg aggtggacgg cgtgctgcgc 420  
 ggccagtcca gcatggccct ggagtgtccc ggcggtcgcc acctgacctg ccacctgcac 480  
 accacctacc gctccaagaa gcccgctccc gccctgaaga tgccccgctt ccacttcgag 540  
 gaccaccgca tcgagatcct ggaggaggtg gagaagggca agtgctacaa gcagtacgag 600  
 gccgccgtgg gccgctactg cgacgccgcc ccctccaagc tgggccacaa ctga 654

<210> 24  
 <211> 232  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> non-aggregating mutant

<400> 24  
 Met Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Arg Thr Thr Ile Glu  
 1 5 10 15  
 Gly Thr Val Asn Gly His Tyr Phe Lys Cys Thr Gly Lys Gly Glu Gly  
 20 25 30  
 Asn Pro Leu Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly  
 35 40 45  
 Gly Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr  
 50 55 60  
 Gly Ser Lys Ala Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe  
 65 70 75 80  
 Lys Gln Ser Leu Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr  
 85 90 95  
 Glu Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly  
 100 105 110

Asp Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala  
           115                          120                          125  
 Asp Gly Pro Val Met Gln Asn Lys Ala Gly Arg Trp Glu Pro Ser Thr  
           130                          135                          140  
 Glu Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Ser Met  
   145                          150                          155                          160  
 Ala Leu Glu Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr  
                           165                          170                          175  
 Thr Tyr Arg Ser Lys Lys Pro Ala Ser Ala Leu Lys Met Pro Gly Phe  
                           180                          185                          190  
 His Phe Glu Asp His Arg Ile Glu Ile Leu Glu Glu Val Glu Lys Gly  
           195                          200                          205  
 Lys Cys Tyr Lys Gln Tyr Glu Ala Ala Val Gly Arg Tyr Cys Asp Ala  
           210                          215                          220  
 Ala Pro Ser Lys Leu Gly His Asn  
   225                          230

<210> 25

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> non-aggregating mutant fragment

<400> 25

Met Arg Ser Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys Val  
   1                          5                          10                          15  
 Arg Met Glu Gly Thr Val Asn Gly His Glu  
                           20                          25

<210> 26

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> non-aggregating mutant fragment

<400> 26

Met Ser Cys Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Gln Val  
   1                          5                          10                          15  
 Arg Met Glu Gly Thr Val Asn Gly His Glu  
                           20                          25

<210> 27

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> non-aggregating mutant fragment

<400> 27

Met	Ala	Gln	Ser	Lys	His	Gly	Leu	Thr	Lys	Glu	Met	Thr	Met	Lys	Tyr
1				5					10					15	
Arg	Met	Glu	Gly	Cys	Val	Asp	Gly	His	Lys						
			20					25							

<210> 28

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> non-aggregating mutant fragment

<400> 28

Met	Ala	His	Ser	Lys	His	Gly	Leu	Lys	Glu	Glu	Met	Thr	Met	Lys	Tyr
1				5					10					15	
His	Met	Glu	Gly	Cys	Val	Asn	Gly	His	Lys						
			20					25							

<210> 29

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> non-aggregating mutant fragment

<400> 29

Met	Ala	Leu	Ser	Asn	Lys	Phe	Ile	Gly	Asp	Asp	Met	Lys	Met	Thr	Tyr
1				5					10					15	
His	Met	Asp	Gly	Cys	Val	Asn	Gly	His	Tyr						
			20					25							

<210> 30

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> non-aggregating mutant fragment

<400> 30



Met Ala Ser Phe Leu Lys Lys Thr Met Pro Phe Lys Thr Thr Ile Glu  
 1 5 10 15  
 Gly Thr Val Asn Gly His Tyr  
 20